## WHAT IS CLAIMED IS:

	1		1.	A method of identifying an exon in a eukaryotic genomic fragment, the			
"He" 4.1.10 '15.	2	method comprising:					
	3		expre	essing a population of subsequences of the genomic fragment in a phage			
	4 display library, wherein the population comprises protein-encoding subsequences a						
	5	noncoding subsequences;					
	6	screening the phage display library with a binding partner to identify an					
	7	expressed	expressed subsequence that specifically binds to the binding partner; and				
	8		mapping the expressed subsequence to the physical location in the genomic				
	9	fragment,	fragment, thereby identifying the exon.				
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	2	enzyme or a receptor.					
	1	~1	3.	The method of claim 2, wherein the binding partner is an antibody.			
	1	1,0	4.	The method of claim 3, wherein the antibody is a single chain			
	2	antibody.					
	1		5.	The method of claim 1, wherein the hinding neutron is assumed to a			
	2	nhage dis	ع. play library	The method of claim 1, wherein the binding partner is expressed by a			
	_	phage dis	play norary	<b>,</b>			
	1		6.	The method of claim 5, wherein the phage display library is an			
	2	antibody <sub>l</sub>	antibody phage display library generated using mRNA isolated from a stimulated B cell or a				
	3	naïve B co	ell.				
	1		7.	The method of claim 6, wherein mRNA isolated from the stimulated B			
	2	cell is mR	NA isolate		נה זה בי		
	3		immunized with a composition comprising the protein epitope encoded by the genomic				
	4		sequence or a nucleic acid encoding the protein epitope.				
	1		8.	The method of claim 1, wherein the expressed subsequences are from			
	2	about 100 base pairs to about 300 base pairs in length.					
	1		9.	The method of claim 1, wherein the genomic fragment is from a			
	2	mammalis	an genome	· · ·			

1	10.	The method of claim 1, further wherein the exon is abnormally			
2	expressed in a cell of an individual with a disease or condition.				
1	11.	The method of claim 10, wherein the cell has a genomic translocation			
2	involving the exon sequence.				
1	12.	The method of claim 10, wherein the disease is cancer.			
1	13.	The method of claim 1, further comprising a step of enriching for			
2	phage expressing subsequences of the genomic fragment that are exons.				
1.	14.	The method of claim 13, wherein the step of enriching comprises			
2	incubating the phage	library with a binding partner specific for a peptide encoded by a			
3	subsequence that does not encode a peptide in vivo, and removing phage expressing the				
4	peptide from the library.				
1	15.	The method of claim 14, wherein the subsequence that does not encode			
2	a peptide in vivo is a				
-	a popular iii vivo is a				
1	16.	The method of claim 15, wherein the repetitive sequence is an Alu			
2	sequence or a Kpn se	quence.			
1	17.	A phage display library comprising phage that express a population of			
2	subsequences of a eukaryotic genomic fragment, wherein the population comprises protein				
3	coding subsequences and noncoding subsequences.				
1	18.	The phage display library of claim 11, wherein the eukaryotic genomic			
2	fragment is from a m	ammalian genome.			
1	19.	The phage display library of claim 17, wherein the library is			
2	constructed using a pBPM-1 vector.				
1	20.	The phage display library of claim 17, wherein the expressed			
2	subsequences are from	m about 100 base pairs to about 300 base pairs in length.			
1	21.	A phage expression vector comprising a polylinker region, an out-of-			
2	frame pIII gene, and	at least one non-pallindromic rare cutting restriction enzyme site located			
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- in the polylinker site, wherein the non-pallindromic rare cutting restriction enzyme site is not 3 4 located outside the polylinker region, and a selection tag encoding sequence. 1 22. The phage expression vector of claim 21, wherein the non-2 pallindromic rare cutting restriction enzyme site is an SfiI site. 1 23. The phage expression vector of claim 21, wherein the selection tag is 2 an epitope tag selected from the group consisting of a polyhistidine tag or a myc tag. 1 24. The phage expression vector of claim 21, wherein the selection tag is an 2 antibiotic resistance polypeptide. A method of identifying an exon in a genomic fragment, the method 1 25. comprising: expressing a population of subsequences of the genomic fragment in a phage display library, wherein the population comprises protein-encoding subsequences and noncoding subsequences; enriching for phage expressing subsequences of the genomic fragment that are exons; screening the phage display library with a binding partner to identify an expressed subsequence that specifically binds to the binding partner; and mapping the expressed subsequence to the physical location in the genomic fragment, thereby identifying the exon. 1 26. The method of claim 25, wherein the step of enriching comprises 2 incubating the phage library with a binding partner specific for a peptide encoded by a 3 subsequence that does not encode a peptide in vivo, and removing phage expressing the 4 peptide from the library. 1 27. The method of claim 26, wherein the subsequence that does not encode 2 a peptide in vivo is a repetitive sequence.
  - 28. The method of claim 25, wherein the expressed subsequences are from about 100 base pairs to about 300 base pairs in length.

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